

CTCGAGGACAGTGACCTGGGAGTGAGTACAAGGTGAGGCCACCACTCAGGGT
GCCAGCTCCAAGCGGGTCACAGGGACGAGGGCTGCGGCCATCAGGAGGCCCT
GCACACACATCTGGGACACGCGCCCCCGAGGGCCAGTTCACCTCAGTGCGCC
TCATTCTCCTGCACAAAAGCGCCCCCATCCTTTCTTCACAAGGCTTTTCGTGG
AAGCAGAGGCGTCGATGCCCAGTACCCTCTCCCTTTCCCAGGCAACGGGACC
CCAAGTTTGCTGACTGGGACCACCAAGCCACGCATGCGTCAAGAGTGAGAGT
CCGGGACCTAGGCAGGGGGCCCTGGGGTTGGGCCTGAGAGAGAAGAGAACCTC
CCCCAGCACTCGGTGTGCATCGGTAGTGAAGGAGCCTCACCTGACCCCCGCT
GTTGCTCAATCGACTTCCCAAGAACAGAGAGAAAAGGGAAGTTCAGGGCGG
CCCGGGCCTCCTGGGGGTTCCCAACCCATTTTTAGCTGAAAGCACTGAGGCA
GAGCTCCCCCTACCCAGGCTCCACTGCCCCGGCACAGAAATAACAACCACGGT
TACTGATCATCTGGGAGCTGTCCAGGAATTC

FIG._1A

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1 GCTGGGCTAA ACTGGGCTAG CCTGAGCTGG GCTGAACTGG GCTGCTGGGC
51 TGGACTGGGT AAGCTGGGCT GAGCTGGGTT GGGTGGAAT GGGCTGAGCT
101 GAGCTAGGCT AACTGGGTT TGGCTGGGCT GGGCTGGGCT GGG

FIG._2B

1 GGTTTGGCTG GGCTGGGCTG GGCTGGGCTG GGTTGAGCTG AGCGGGTTGG
51 GTTAGACTGG GTCAAAGTGG TTCAGC

FIG._2C

+

GERMLINE & LOCUS

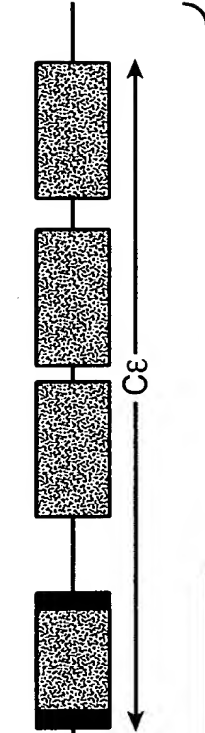
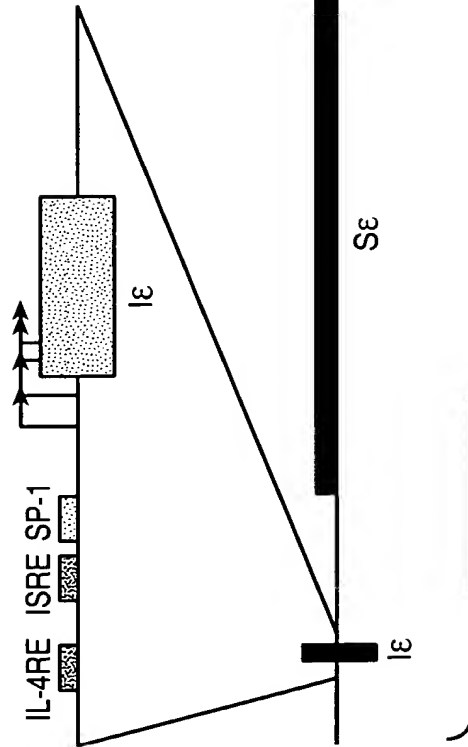
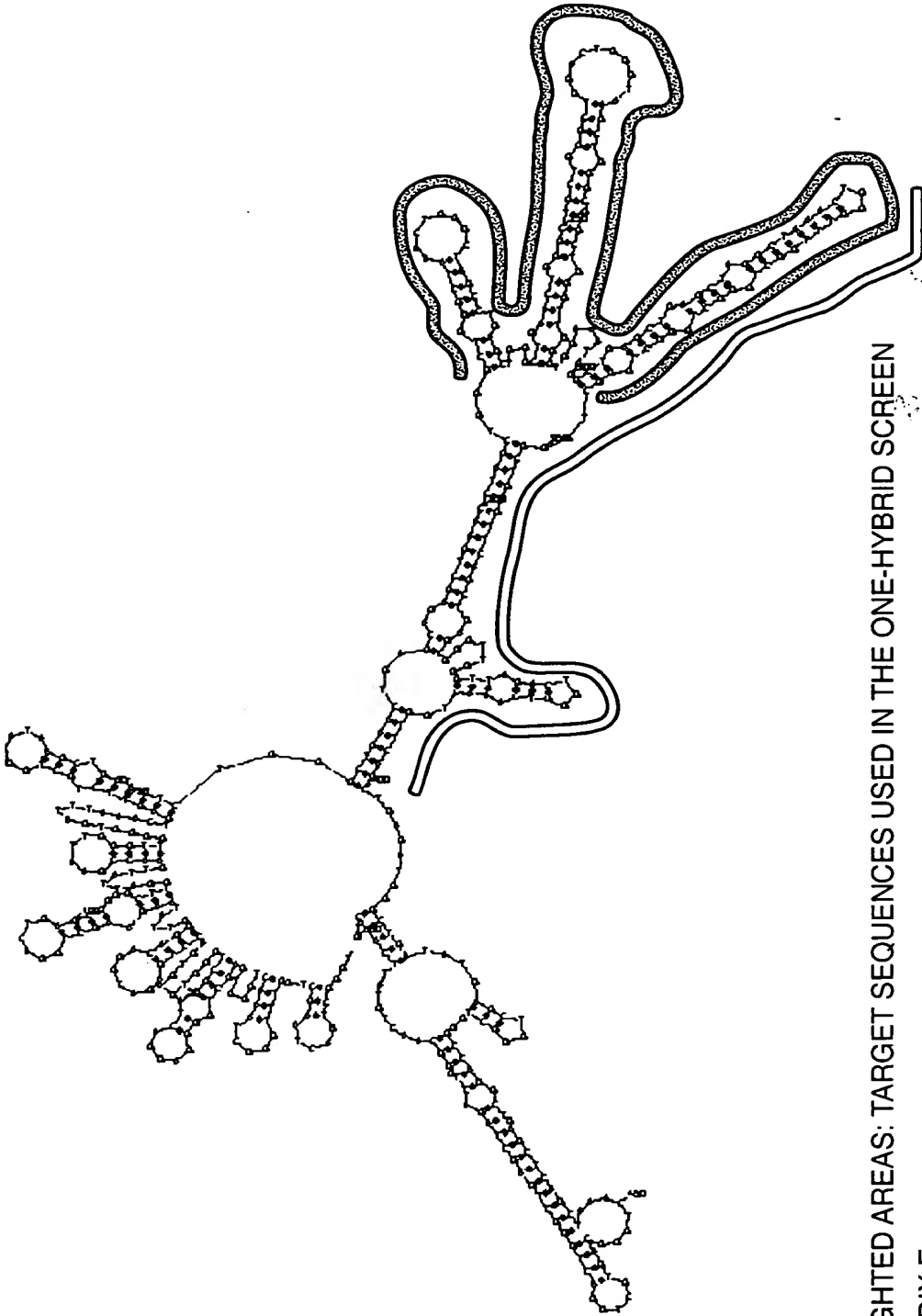


FIG. 1B

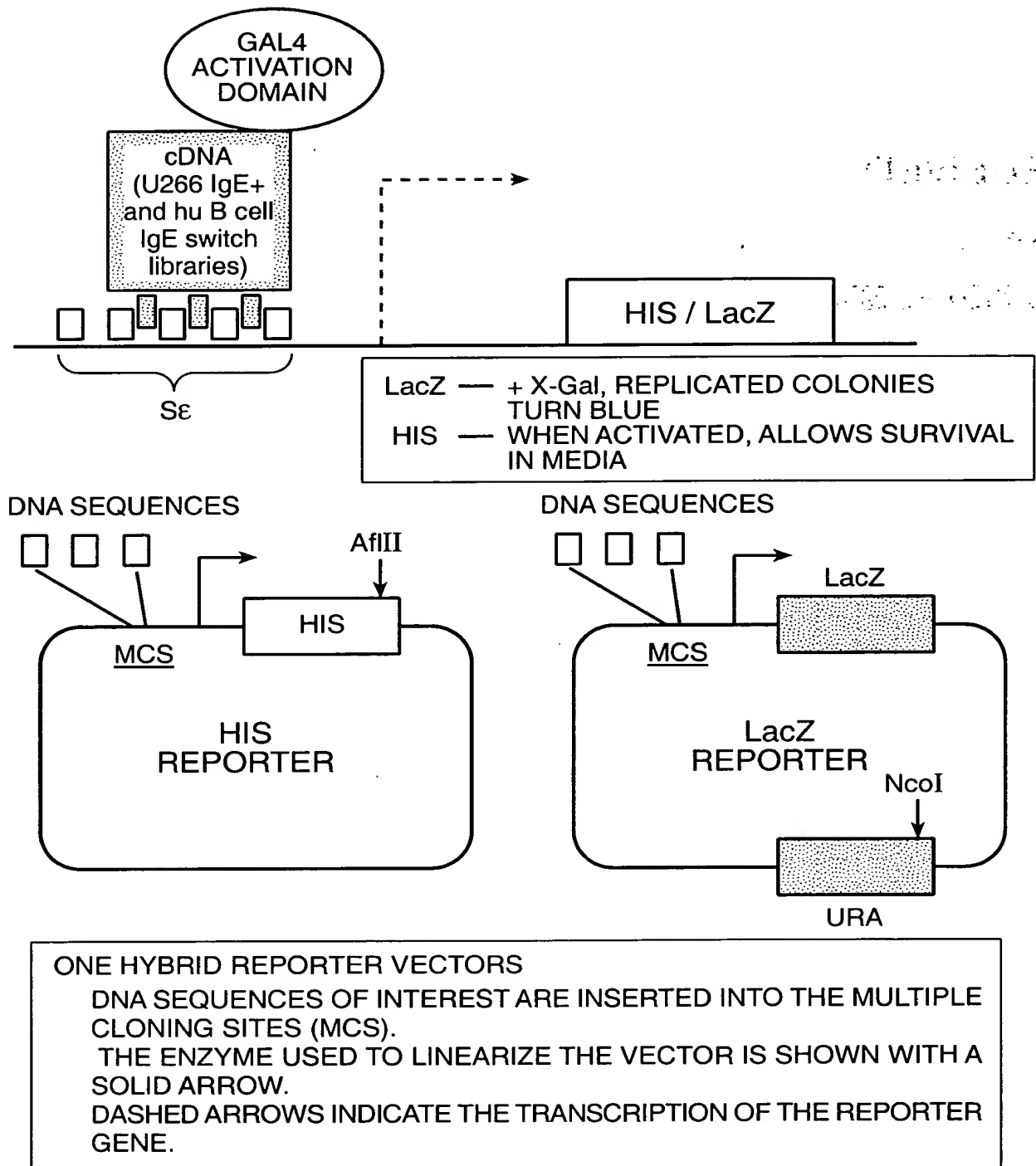
LOW ENERGY DNA FOLDING OF THE S_ε REGION



HIGHLIGHTED AREAS: TARGET SEQUENCES USED IN THE ONE-HYBRID SCREEN
APPENDIX E

FIG._2A

YEAST ONE-HYBRID SCREENING



APPENDIX F

FIG. 3

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IL-4 INDUCTION OF GERMLINE ϵ mRNA IN THE
IgM + B CELL LINES: CA-46, MC-116 AND DND39

DND39 + IL-4

DND39 - IL-4

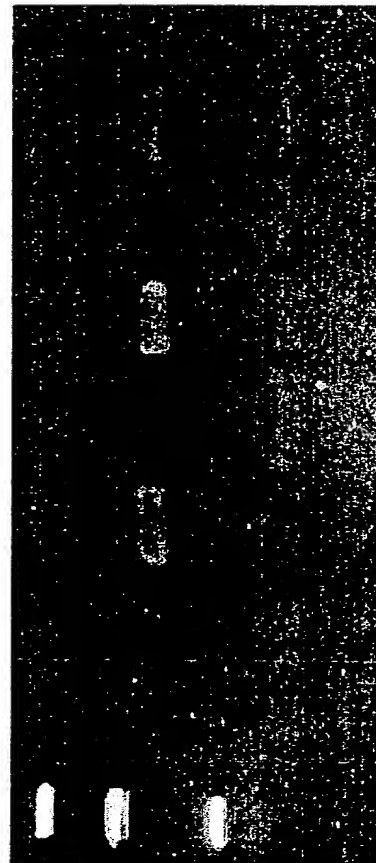
MC-116 + IL-4

MC-116 - IL-4

CA-46 + IL-4

CA-46 - IL-4

NEG. CONT.



246bp

123bp

CELLS WERE INCUBATED FOR 48 HRS. IN 300 U / ml OF h-IL-4.
RT-PCR WAS PERFORMED USING PRIMERS SPECIFIC FOR THE GERMLINE
 ϵ EXON AND THE 5'-END OF THE C ϵ CH1 EXON (PREDICTED SIZE ~ 200 bp).

APPENDIX G

FIG._4

APPROACHES TO GENERATE GERMLINE ϵ PROMOTER KNOCK-IN REPORTER CELL LINES

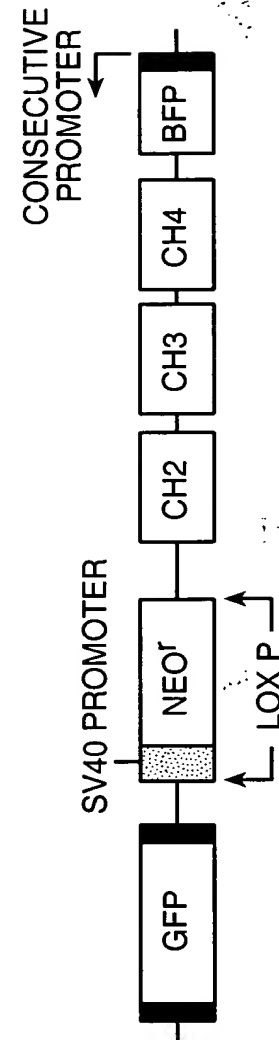
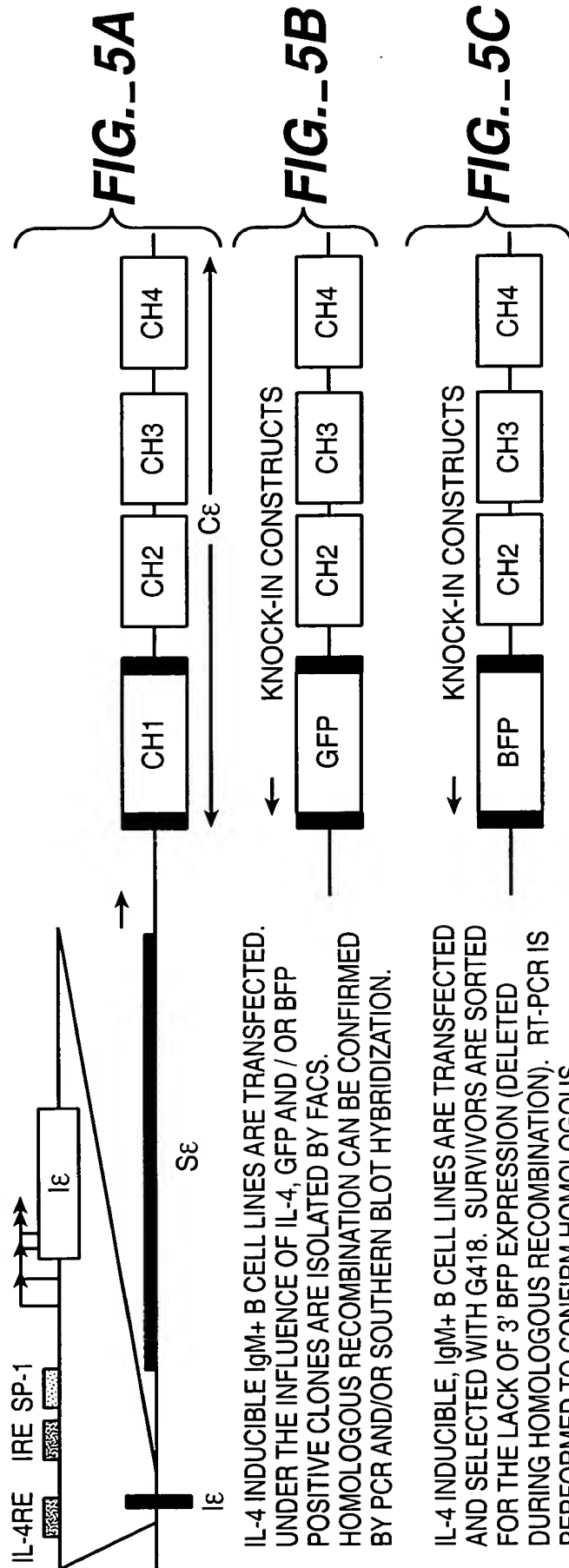
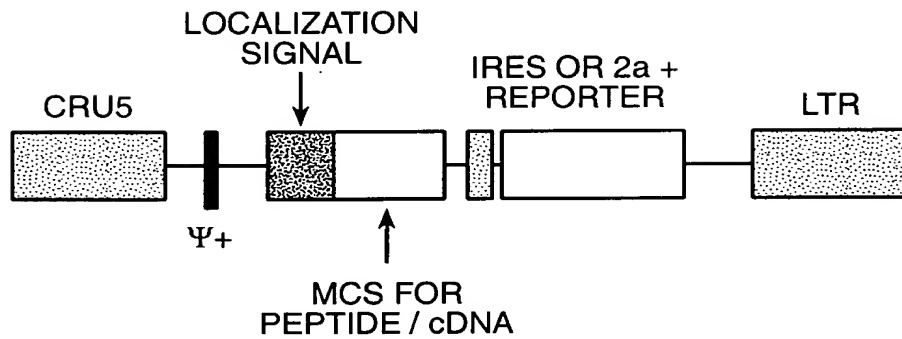


FIG. 5D

APPENDIX A

RIGEL BASE VECTOR



ALL COMPONENTS ARE UNIQUELY CASSETTED FOR FLEXIBILITY

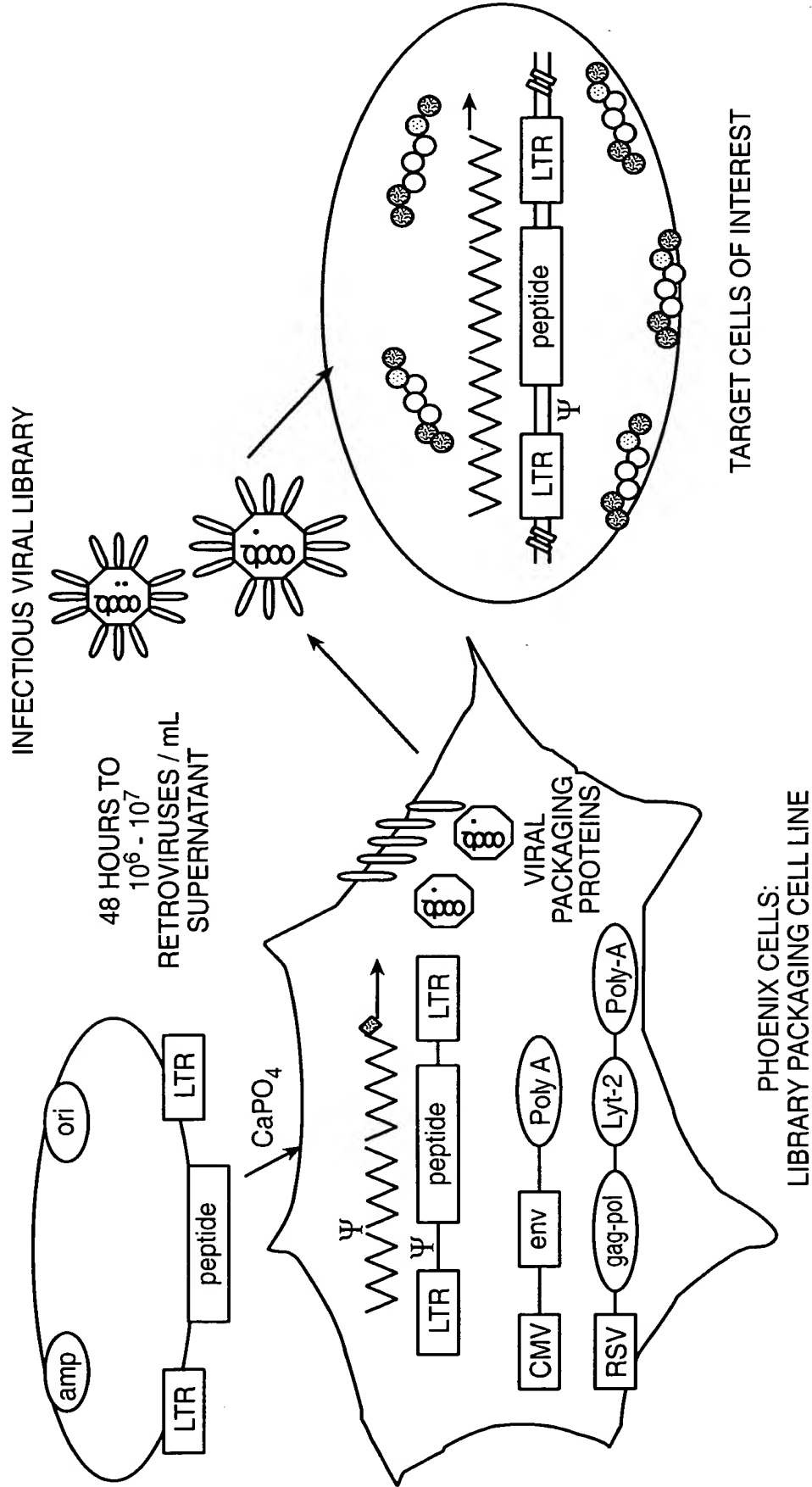
CRU5, MODIFIED LTR
LTR, LONG TERMINAL REPEAT
 $\Psi+$, PACKING SIGNAL
LOCALIZATION SIGNAL: NUCLEAR, CELL MEMBRANE, GRANULAR
MCS, MULTIPLE CLONING SITE
IRES, INTERNAL RIBOSOME ENTRY SITE
2a, SELF-CLEAVING PEPTIDE

APPENDIX I

FIG._6

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PROTOCOL FOR TRANSFECTION OF PHOENIX CELLS AND INFECTION OF NONADHERENT TARGET CELLS



APPENDIX I

FIG. 7

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ε HEAVY CHAIN GFP / BFP KNOCK-IN CELL LINE

U266 ε HEAVY CHAIN

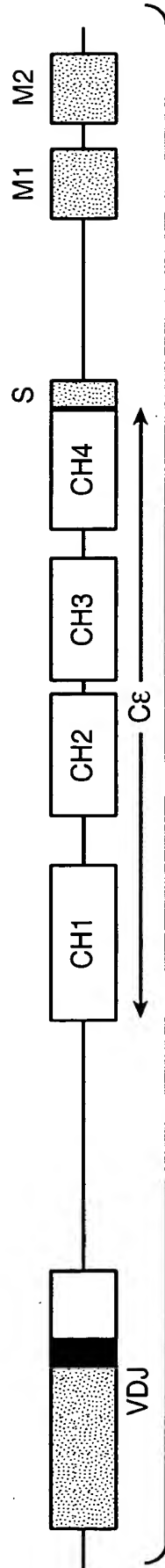
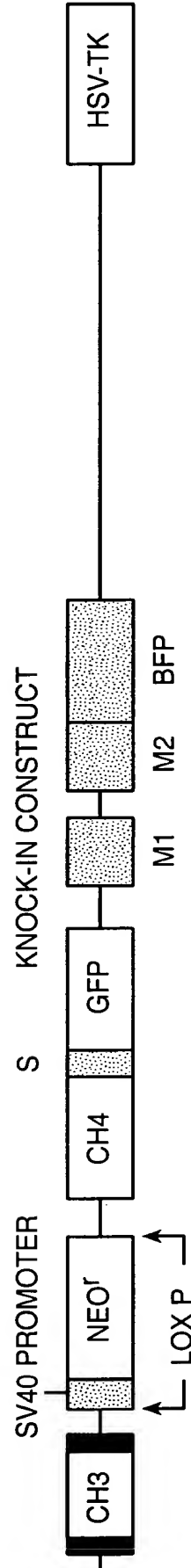


FIG. 8A



S, SECRETORY EXON
 GFP, GREEN FLUORESCENT PROTEIN
 BFP, BLUE FLUORESCENT PROTEIN
 Neo^r, NEOMYCIN RESISTANCE GENE
 VDJ, V REGION EXON
 CH 1, 2, 3, 4, CONSTANT REGION DOMAIN EXONS
 M1, M2, MEMBRANE EXONS
 HSV-TK, HERPES SIMPLEX VIRUS-THYMIDINE KINASE

U266 CELLS ARE TRANSFECTED AND SELECTED WITH G418. SURVIVORS ARE TREATED WITH GANCICLOVIR (HSV-TK DELETED DURING HOMOLOGOUS RECOMBINATION). RT-PCR IS PERFORMED TO CONFIRM HOMOLOGOUS RECOMBINATION. THOSE CLONES ARE TRANSFECTED WITH *cre* TO REMOVE THE SV40 NEOMYCIN RESISTANCE GENE.

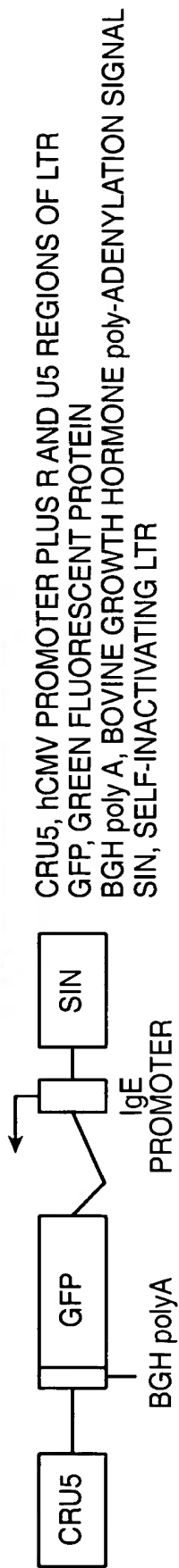
APPENDIX D

FIG. 8B

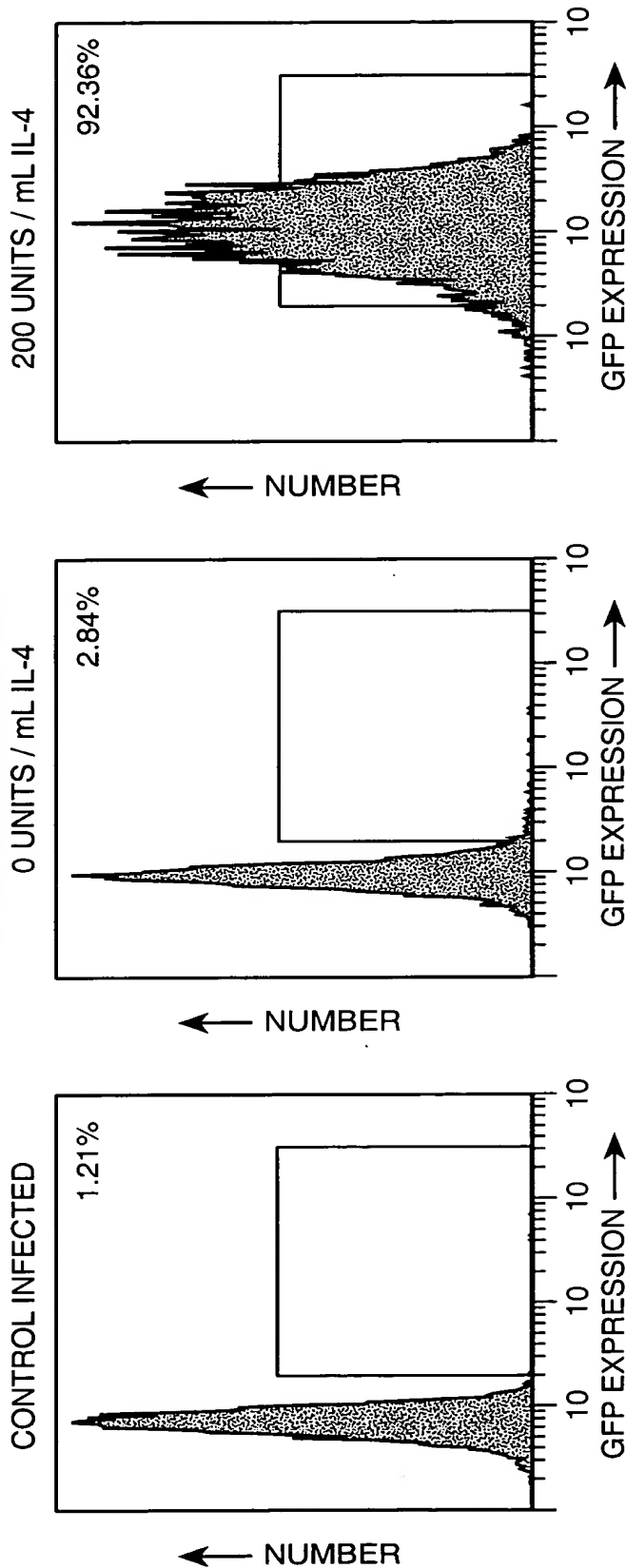
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IL-4 INDUCIBLE ϵ PROMOTER REPORTER CELL LINE

REPORTER CONSTRUCT



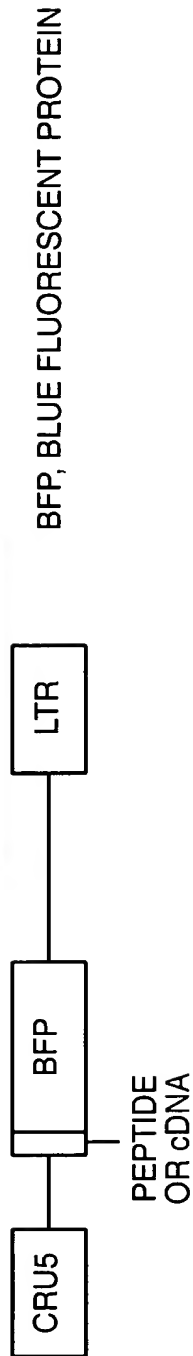
IL-4 INDUCED REPORTER



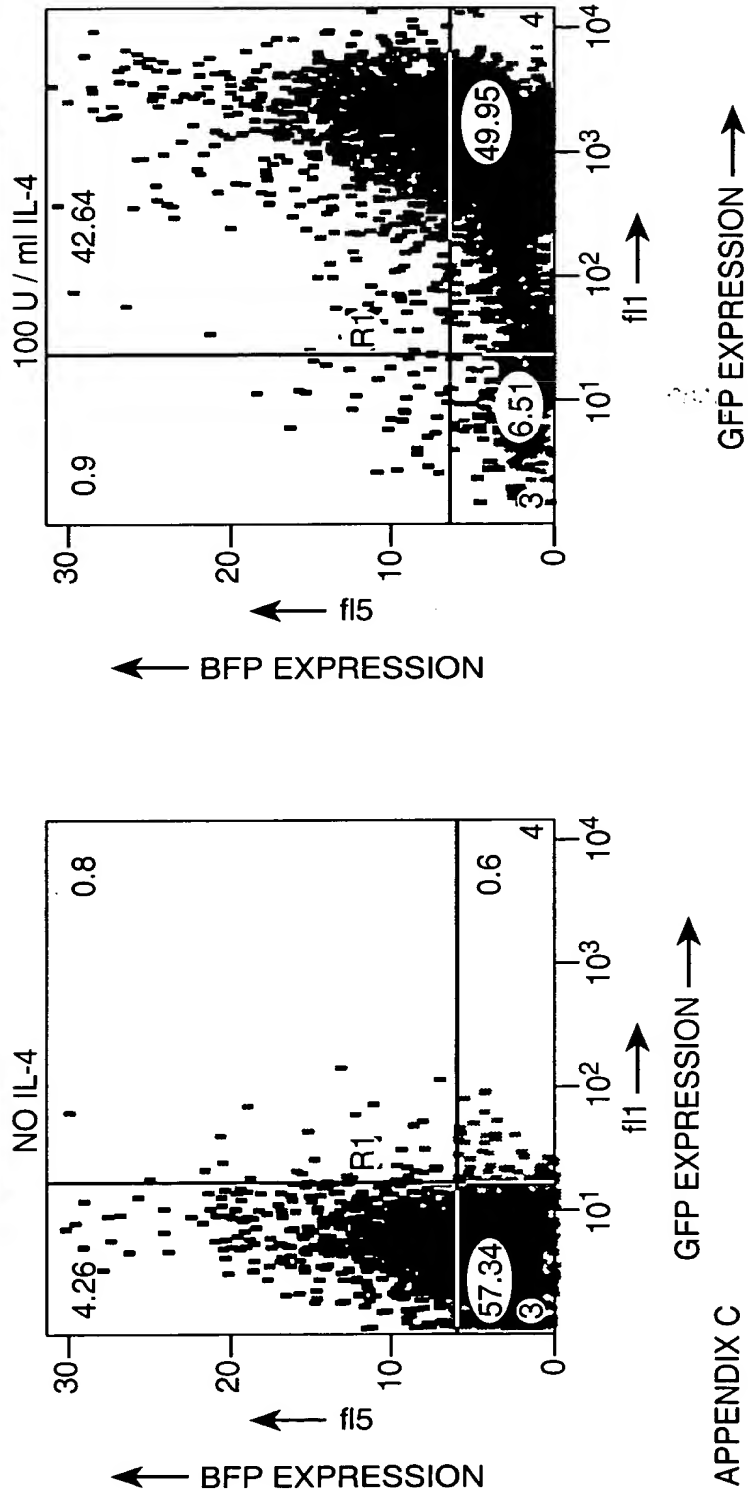
APPENDIX C

FIG._9A

REPORTER LINE INFECTED WITH BFP CONSTRUCT

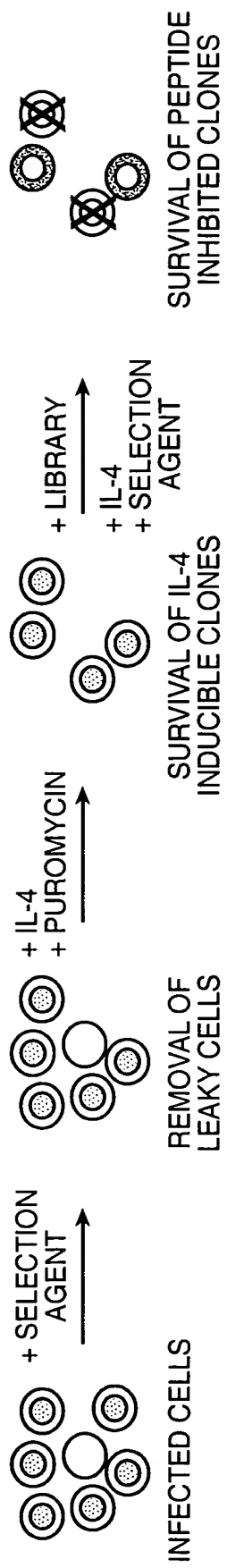
LIBRARY CONSTRUCT

BFP, BLUE FLUORESCENT PROTEIN

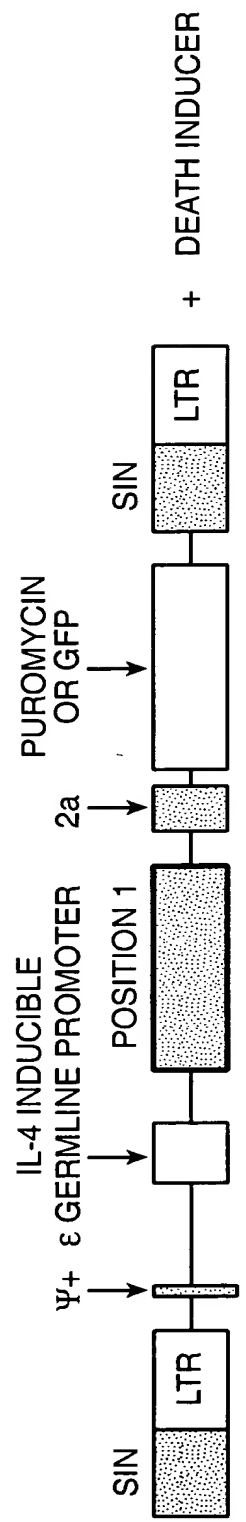
FACS PROFILE OF CELLS WITH BOTH REPORTER AND PEPTIDE LIBRARY**FIG._9B**

+

SCREEN FOR PEPTIDE INHIBITORS OF THE GERMLINE ϵ PROMOTER



SURVIVAL CONSTRUCT



POSITION 1

FAS CHIMERIC RECEPTOR*
 *(MOUSE FASK EXTERNAL / MOUSE CD8 EXTERNAL + HUMAN TRANSMEMBRANE AND CYTOPLASMIC DOMAINS)

HSV-TK
 P450 2B1
 p21 PEPTIDE

SELECTION AGENT

α FAS
 GANCICLOVIR
 CYCLOPHOSPHAMIDE
 NONE (SELF SELECTION)

ALL COMPONENTS ARE CASSETTED FOR FLEXIBILITY

APPENDIX D

FIG..10

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1-845 CMV promoter/R/U5 5' LTR
1322 GAG ATG-ATC mutation
850-2100 extended Ψ region
2146-2173 two Bstx1 peptide cloning sites
2205-2723 ECMV IRES (cloned as EcoR1/MscI fragment from
pCITE-4a [Novagen])
2746-3465 GFP coding region
3522-4115 3' LTR
4122-6210 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATCC
CAAACCTCAAATATATAAAGCATTTGACTTGTCTATGCCCTAGTTATTAATAGTAATCAA
TTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAA
ATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTTGACGTCAATAATGACGTATG
TTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGGTGGAGTATTTACGGT
AAACTGCCCACCTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTC
CTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGC
AGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCA
TTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACCTCCGCCCCATTGACGCAAAATGGGCGGTAGGCATGTACGGTGGGAGGTCTATATAA
GCAGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACT
GAGTCGCCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGACAGTTGCATCCGACTTGTGGT
CTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTT
CATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCACCG
GGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGACTGA
TTTTATGCGCCTGCGTCCGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGG
TGGAACCTGACGAGTTCGGAACACCCGGCCGCAACCCTGGGAGACGTCCAGGGGACTTCGG
GGGCCGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGATCGTTTTGGACTCTTTGGTG
CACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGACGAGAACCTAAACAGTTCC
CGCCTCCGTCTGAATTTTTTGCTTTTCGGTTTGGGACCGAAGCCGCGCCGCGCGTCTTGTCT
GCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATA
TCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCAGTGGAAAGATG
TCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCT
GCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAG
ACCTCATCACCCAGGTTAAGATCAAGGTCTTTTTCACCTGGCCCGCATGGACACCCAGACC
AGGTCCCCTACATCGTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGC
CCTTTGTACACCTAAGCCTCCGCCTCCTCTTCCCTCCATCCGCCCCGTCTCTCCCCCTTG
AACCTCCTCGTTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTCCTTCTCTAG
GCGCCCCCATATGGCCATATGAGATCTTATATGGGGCACCCCCGCCCCCTTGTAACCTTCC
CTGACCCTGACATGACAAGAGTTACTAACAGCCCCCTCTCTCCAAGCTCACTTACAGGCTC
TCTACTTAGTCCAGCACGAAGTCTGGAGACCTCTGGCGGCAGCCTACCAAGAACAACCTGG
ACCGACCGGTGGTACCTCACCTTACCGAGTCGGCGACACAGTGTGGGTCCGCCGACACC
AGACTAAGAACCTAGAACCTCGCTGGAAAGGACCTTACACAGTCCTGCTGACCACCCCCA
CCGCCCTCAAAGTAGACGGCATCGCGCTTGGATACACGCCGCCACGTGAAGGCTGCCGA
CCCCGGGGGTGGACCATCTCTAGACTGCCGGATCTCGAGGGATCCACCACCATGGACCC
CCATTAAATTGGAATTCCTGCAGCCCGGGGGGATCCACTAGTTCTAGAGCGAATTAATTC

FIG. 11A-1

GGTTATTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTG
TCTTCTTGACGAGCATTCTAGGGGTCTTTCCCTCTCGCCAAAGGAATGCAAGGTCTGT
TGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAG
CGACCCTTTGCAGGCAGCGGAACCCCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGC
CACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCAGTGCCACGTTGTGAGTTGGA
TAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATG
CCCAGAAGGTACCCCATTTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTACAT
GTGTTTAGTCGAGGTTAAAAACGTCTAGGCCCCCGAACCACGGGGACGTGGTTTTCCT
TTGAAAAACACGATGATAATATGGGGGATCCACCGGTGCGCCACCATGGTGAGCAAGGGCG
AGGAGCTGTTCAACGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCC
ACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGA
AGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGA
CCTACGGCGTGACGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCA
AGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA
ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGC
TGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC
ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAC
TCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGA
ACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGT
CCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTTGCTGGAGTTCGTGA
CCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTAAAGCGGCCGCTCGACGA
TAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTA
GGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAAATACATAACTGA
GAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACA
GGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTG
AATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAA
CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTC
CAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTTC
CTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
TCACTCGGGGCGCCAGTCCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAA
ACCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGA
GTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTCCGACTTGTGGTCTCGCTGCCTTGG
GAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCACATGCAGCATGTAT
CAAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGCGCTCTTCCGCTTCCTCGCT
CACTGACTCGCTGCGCTCGGTCTGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC
GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAGG
CCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG
CCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG
ACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC
CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGT
GCACGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTC
CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC

FIG. 11A-2

TAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT
TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAA
GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG
GTCTGACGCTCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGAGATTATCAAA
AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTGCGCAAATCAATCTAAAG
TATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTC
AGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGG
TCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAG
TAGTTCGCCAGTTAATAGTTTGCAGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTG
ACGCTCGTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTAC
ATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTGAG
AAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTAC
TGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTG
AGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGC
GCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAAC
CTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTG
ATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAA
TGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTT
TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG
TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTT

FIG. 11A-3

1-845 CMVpromoter/R/U5 5' LTR
1322 GAG ATG-ATC mutation
850-2100 extended ψ r gion
2151-2865 GFP coding region
2866-2894 GGGSGGG linker
2895-2952 FMDV 2a cleavage sequence
2953-3004 Bstx1/Bstx1/HinD3/Hpa1/Sal1/Not1 polylinker
3052-3645 3' LTR
3652-5715 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATC
CCAAACTCAAATATATAAAGCATTTGACTTGTTCTATGCCCTAGTTATTAATAGTAATC
AATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAACTTACGG
TAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTGACGTCAATAATGACG
TATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTT
ACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTA
TTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGG
GACTTTCTTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCG
GTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTC
TCCACCCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCA
AAATGTCTGTAACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
GGTCTATATAAGCAGAGCTCAATAAAAGAGCCACAAACCCCTCACTCGGGGCGCCAGTC
CTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCTCTTGACAGTTGCA
TCCGACTTGTGGTCTCGCTGTTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGT
CAGCGGGGGTCTTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACC
ACCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTC
TAGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGT
ATCTGGCGGACCCGTGGTGGAAC TGACGAGTTTCGGAACACCCGGCCGCAACCCTGGGAG
ACGTCCCAGGGACTTCGGGGGCGGTTTTTGTGGCCCGACCTGAGTCCAAAAATCCCGAT
CGTTTTTGACTCTTTGGTGACACCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGA
CGAGAACCTAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGGACCGAA
GCCGCGCCGCGCGTCTTGCTGCTGACGATCGTTCTGTGTTGTCTCTGTCTGACTGTG
TTTCTGTATTTGTCTGAAAATATCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTT
GACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCA
AGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCCGATGG
CCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTC
ACCTGGCCCCGCATGGACACCCAGACCAGGTCCCTTACATCGTGACCTGGGAAGCCTTGG
CTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTT
CCTCCATCCGCCCCGTCTCTCCCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCCTC
CCTTTATCCAGCCCTCACTCCTTCTTAGGCGCCCCCATATGGCCATATGAGATCTTAT
ATGGGGCACCCCCGCCCCCTTGTAACCTTCCCTGACCCTGACATGACAAGAGTTACTAAC
AGCCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAG
ACCTCTGGCGGCAGCCTACCAAGAACAACCTGGACCGACCGGTGGTACCTCACCTTACC
GAGTCGGCGACACAGTGTGGGTCCGCGGACACCAGACTAAGAACCTAGAACCTCGCTGG
AAAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATCGC
AGCTTGATACACGCGCCGACGTTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTA
GACTGCCGGATCTCGAGGGATCCACCATGGTGAGCAAGGGCGAGGAGCTGTTACCGGG

FIG. 11B-1

GTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC
CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCA
CCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCCAG
TGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCC
CGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCC
GCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATC
GACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCA
CAACGTCATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCC
GCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCC
ATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCGCCCT
GAGCAAAGACCCCCAACGAGAAGCGCGATCACATGGTCTCTGCTGGAGTTCGTGACCGCCG
CCGGGATCACTCTCGGCATGGACGAGCTGTACAAGGAATTCGGAGGTGGCAGCGGTGGC
GGTCAGCTGTTGAATTTTGACCTTCTTAACTTGCGGGAGACGTCGAGTCCAACCCTGG
GCCACCACCACCATGGAAGCTTCCATTAAATTGGTTAACGTCGACGCGGCCGCTCGAC
GATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCACCT
GTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAA
CTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCC
AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAA
CAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCA
ATCAGTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGC
CCACAACCCCTCACTCGGGGCGCCAGTTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
GTATCCAATAAACCCCTCTTGCAAGTTGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAG
GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTCCGACTTGTGGT
CTCGCTGCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTCA
CATGCAGCATGTATCAAAATTAATTTGGTTTTTTTTCTTAAGTATTTACATTAAATGGC
CATAGTTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGCGCT
CTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTCTCGGTGCGGCGAGCGGTA
TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA
GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGG
CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG
AGGTGGCGAAACCCGACAGGACTATAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCT
CGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTT
CGGGAAGCGTGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTAGCCCGACCGCTGCGCCTT
ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG
CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG
AAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG
CTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCT
CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAACTCACG
TTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATT
AAAAATGAAGTTTTCGCAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGT
TACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCAT
AGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCC
CCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATA

FIG. 11B-2

AACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCAT
CCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACACGCTCGTCGTTTGGTATGGCT
TCATTACAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAA
AAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGT
TATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCAFGCCATCCGTAAGA
TGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCG
ACCGAGTTGCTCTTGCCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTT
TAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCG
CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAGTATCTTCAGCATCTTT
TACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGG
GAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTCAATATTATTGA
AGCATTTATCAGGGTTATTGTCTCATGACATTAACCTATAAAAATAGGCGT

FIG. 11B-3

1-845 CMVpormoter/R/U5 5' LTR
1322 GAG ATG-ATC mutation
850-2100 extended ψ region
2146-2173 two Bstx1 peptide cloning sites
2173-2214 Eor1/Apa1/Hpa1/Not1 polylinker
2262-2855 3' LTR
2855-4901 pGEM backbone (pUC origin, ampR)

ATCACGAGGCCCTTTCGTCTTCAAGAACAGCTTTGCTCTTAGGAGTTTCCTAATACATC
CCAAACTCAAATATATAAAGCATTGACTTGTTCTATGCCCTAGTTATTAATAGTAATC
AATTACGGGGTCATTAGTTCATAGCCATATATGGAGTTCGCGGTTACATAACTTACGGT
AAATGGCCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTTGACGTCAATAATGACGT
ATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTA
CGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTAT
TGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGG
TTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCGAAGTCT
CCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAA
AATGTCGTAACAACCTCCGCCCCATTGACGCAATGGGCGGTAGGCATGTACGGTGGGAG
GTCTATATAAGCAGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGGGCGCCAGTCC
TCCGATTGACTGAGTCGCCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCAAGTGCAT
CCGACTTGTGGTCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTC
AGCGGGGGTCTTTTCATTTGGGGGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCA
CCGACCCACCACCGGGAGGTAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCT
AGTGTCTATGACTGATTTTATGCGCCTGCGTCGGTACTAGTTAGCTAACTAGCTCTGTA
TCTGGCGGACCCGTGGTGGAACTGACGAGTTCGGAACACCCGGCCGCAACCCCTGGGAGA
CGTCCAGGGACTTCGGGGGCGGTTTGTGTTGGCCGACCTGAGTCCAAAAATCCCGATC
GTTTTGGACTCTTTGGTGCACCCCCCTTAGAGGAGGGATATGTGGTTCTGGTAGGAGAC
GAGAACCCTAAACAGTTCCCGCCTCCGTCTGAATTTTGGCTTTCGGTTTGGGACCGAAG
CCGCGCCGCGCGTCTTGTCTGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGT
TTCTGTATTTGTCTGAAAAATATCGGCCCGGGCCAGACTGTTACCACTCCCTTAAGTTTG
ACCTTAGGTCACTGGAAAGATGTGCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAA
GAAGAGACGTTGGGTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGC
CGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTTTTCA
CCTGGCCCGCATGGACACCCAGACAGGTCCCTTACATCGTGACCTGGGAAGCCTTGGC
TTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCCTCCTCTTC
CTCCATCCGCCCCGTCCTCTCCCCCTTGAACCTCCTCGTTTCGACCCCGCCTCGATCCTCC
CTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCCCCATATGGCCATATGAGATCCTTATA
TGGGGCACCCCCGCCCCCTTGTAACCTTCCCTGACCCTGACATGACAAGAGTTACTAACA
GCCCCCTCTCTCCAAGCTCACTTACAGGCTCTCTACTTAGTCCAGCACGAAGTCTGGAGA
CCTCTGGCGGCAGCCTACCAAGAACAACTGGACCGACCGGTGGTACCTCACCTTACCG
AGTCGGCGACACAGTGTGGGTCCGCCGACACCAGACTAAGAACCCTAGAACCCTCGCTGGA
AAGGACCTTACACAGTCCTGCTGACCACCCCCACCGCCCTCAAAGTAGACGGCATCGCA
GCTTGGATACACGCCGCCACGTGAAGGCTGCCGACCCCGGGGGTGGACCATCCTCTAG
ACTGCCGGATCTCGAGGGATCCACCACCATGGACCCCATTAATTTGAATTCGGGGCC
CAAGCTTTGTAAACGTCGACGCGGCCGCGCTCGACGATAAAATAAAGATTTTATTTAG
TCTCCAGAAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAG
TAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCA

FIG._11C-1

AGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAG
TTCTTGGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGA
TATCTGTGGTAAGCAGTTCTTGGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATG
CGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGA
CCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTT
CGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCC
AGTCCTCCGATTGACTGAGTCGCCCCGGGTACCCGTGTATCCAATAAACCCCTCTTGCACT
TGCATCCGACTTGTGGTCTCGCTGTTCTTGGGAGGGTCTCCTCTGAGTGATTGACTAC
CCGTACGCGGGGGTCTTTCAATTTCCGACTTGTGGTCTCGCTGCCTTGGGAGGGTCTCCT
CTGAGTGATTGACTACCCGTACGCGGGGGTCTTCACATGCAGCATGTATCAAAATTAAT
TTGGTTTTTTTTTCTTAAGTATTTACATTAAATGGCCATAGTTGCATTAATGAATCGGCC
AACGCGCGGGGAGAGGCGGTTTGGCTATTGGCGCTCTTCCGCTTCTCTCGCTCACTGACT
CGCTGCGCTCGGTTCGTTCCGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATA
CGGTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA
AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC
CTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA
TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCT
GCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATA
GCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTG
CACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTC
CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA
GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG
AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTT
GCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT
ACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGAGATT
ATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAGTTTGGCGCAAATCAA
TCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCA
CCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTA
GATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAG
ACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAG
CGCAGAAGTGGTCTTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGA
AGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGCGAACGTTGTTGCCATTGCTACAG
GCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGA
TCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCC
TCCGATCGTTGTCAGAAGTAAGTTGGCCGCAAGTGTATCACTCATGGTTATGGCAGCAC
TGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTAC
TCAACCAAGTCATTCTGAGAATAGTGATGCGGCGACCGAGTTGCTCTTGCCCGGCGTC
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CCCACTCGTGACCCAACTGATCTTCAGCATCTTTTACTTTTACCAGCGTTTCTGGGTG
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GAATACTCATACTCTTCCTTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTC
ATGACATTAACCTATAAAAATAGGCGT

FIG._11C-2

C12ScFas: epsilon-cFas(CD95)-Ires-Hygro-BGH PolyA put into C12s vector backwards so that no leaky transcription happens through the cmv promoter.

atcacgaggcccttctcgcttccaagaacagcttctgctcttaggagtttccctaatacatcccaaaactccaataataataaagc
atctgacttgttctatgccctagttattaatagtaaatcaattacggggtcaattagttcatagcccatataataggagtctccg
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ttcccatagtaaacgccaatagggactttccattgacgtcaatgggtggagtatattacggtaaaactgcccaacttggcagta
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catgacctatgggactttcctacttggcagttacattctacgtattagtcacgtctatcacctattacatggtgatgcggttttggc
agtacatcaatggcggtgatatgggtttgactcacgggatttccaagtctccacccattgacgtcaatggcggttaggcatgtt
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gagtcgccccgggtaccctgtatccaataaaacctcttgcaatttgcaattgcatccgacttgggtctcgctgtccttgggaggg
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ggacacacgaccccaacacgggaggttaagctggccagcaacttatctgtgtctgtccgattgtctagtgcttatgactga
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cgccacgtgaaggctgcgacccccggggttgaccatcctctagactgcccGGATCTCAGAGGATCTTCCCCAGCATGCC

TGCTATTGCTCTCCCAATCCTCCTCCCTTGTCTGCTCCCAACCCACCCAGATAGAAATGACACCTACTCAGACAA

TGCGATGCAATTTCCTCATTTATTAGGAAAGGACAGTGGGAGTGGCACCTTCAGGGTCAAGGAAGCACGGGGAGGG

GCAAACAACAGATGGCTGGCAACTAGAAAGGCACAGTCGAGGCTAGCTTGCCAAACCTACAGTGGGGCTTTTCATTCCC

CCCTTTTCTGGAGACTAAATAAAATCTTTTATTTTatcgatagatcccggtcggcatctactctattccttctgcccctcg
gacgagtgcctggggtcgggttccactatcggcgagtagtctctacacagccatcgggtccagacggcgccgcttctgcggtg
gcgatttgtgtacgcccgcagacagtcccggtccggatcggacgattggtcgcatcgacctgacccctgccccaaagctgcatcatc
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gccgatgcaaatgcccataaacaataacgatctttgtagaaacatcggcgagctatttaccgagggacatatccacg
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tttccacaactatccaaactcacaacgtggcactgggtgtgcccccttgcaggtgtatcttatacacgtggcttttgg
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ccaaccggttTCTGGGACTTGTGTTTCTCTGCAGTTTGTATTGCTGGTTGCTGTGCATGGCTCAAGGGTTCCATGTTTCACAC
GAGGCGCAGCGGAACACAGTGTTTCACAGCCAGGAGAAATCGCAGTAGAAGTCTGGTTTGCACTTGCACTTGGTATTCTGGGT
CAGGGTGCAGTTTGTTCACCTTCTAAACCATGCTCTTTCATCGCAGAGTGTGCATCTTCTGCATTTATCAGCATAAATGGT
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TTTTTACCAGGTTGGCATGGTTGACAGCAAAATGGGCCCTCCTTGATATAATCCTTCTGTAGCAGTTTTTATCAGTTTCATG
AACCCGCCCTCAGCTTTAAACTCTCGGAGATGCTATTAGTACCTTGAGTATGAACCTTAACTGTGAGCCAGCAAGCA

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ggactctCactcttgacgcatgctggtcttgggtcccagtcagcaaaacttggggtcccgctgacctgggaagggagag
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GCTCGACgataAAAAATAAAGATTTTATTAGTCTCCAGAAAAAAGGGGGGAATGAAAGACCCCACTGTAGGTTTGGCAAG
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CCGGAAGCATAAAGTGTAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAAATTGCGTTGCGCTCACTGCCCGCT
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TAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGT
AAAAAGCCCGGCTTGCTGGCGTTTTCCTATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG
GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCGGACCC

FIG.-12C

TGCCGCTTACCGGATACCTGTCCGCCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTC
AGTTCGGGTAGGTCGTTCCAAAGCTGGGCTGTGTGCACGAACCCCGCTTCAGCCCCGACCGCTGCCCTTATCCGG
TAACTATCGTCTTGAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG
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cactcgtgcacccaactgatcttcagcatcttttactttcacccagcgtttctggtgagcaaaaaacaggaaagcaaatg
ccgcaaaaaagggaataaggcgacacgggaaatgttgaatactcatactcttcccttttttcaatatatttgaagcatttat
cagggttatgtctcatgacattaacctataaaaaataggcgt

2.) Ahhhh: epsilon-cFas' (CD8 or mLy2)-Ires-Hygro-BGHpolyA also in C12s backwards

TGCTATTGCTCTCCCAATCCTCCCCCTTGCTGTCTGCCCAACCCCAAGAAATAGAAATGACACCTACTCAGACAA

TGCGATGCAATTCCATTTTATTAGGAAAGGACAGTGGAGTGGCACCTTCCAGGTCAAGGAAGCACGGGGAGGG

GCAAACACAGATGGCTGGCAACTAGAAAGGCACAGTCGAGGCTAGCTTGCCAAACCTACAGTGGGGCTTTCA TTCCC

CCCTTTTCTGGAGACTAAATAAAATCTTTTATTTATcgaatagatcccggctcggcatctactctatctccttggccctcg
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FIG.- 13C

GCTACAGAGTTCTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTGCGCTCTGCTGAAGCC
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FIG.- 13D